

We claim:

1. An isolated nucleic acid sequence which encodes a polypeptide
5 and which is composed of a combination of the nucleic acid sequences of a biosynthesis nucleic acid sequence of the fatty acid or lipid metabolism and one of the following nucleic acids:
 - 10 a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,
 - b) nucleic acid sequences which are derived from the nucleic acid sequence shown in SEQ ID NO: 1 as the result of the degeneracy of the genetic code,
 - 15 c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2 and which have at least 60% homology at the amino acid level,
 - d) a nucleic acid sequence with the sequence shown in SEQ ID NO: 3 or the amino-terminal portion of the coding region of this sequence.
- 25 2. An isolated nucleic acid sequence as claimed in claim 1, wherein a sequence of the following protein groups is used as biosynthesis gene nucleic acid sequence of the fatty acid or lipid metabolism:
 - 30 Acyl-CoA dehydrogenase(s), Acyl-ACP [= acyl carrier protein] desaturase(s), Acyl-ACP thioesterase(s), fatty acid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases and/or fatty acid elongase(s).
 - 35 3. An isolated nucleic acid sequence as claimed in claim 1 or 2, wherein a sequence of the following protein groups is used as biosynthesis gene nucleic acid sequence of the fatty acid or lipid metabolism:
fatty acid acyltransferase(s), Δ4 desaturase, Δ5 desaturase, Δ6 desaturase, Δ9 desaturase, Δ12 desaturase, Δ15 desaturase
45 or a fatty acid elongase.

4. An isolated nucleic acid sequence as claimed in any of claims 1 to 3, wherein the derivatives mentioned under (c) have a homology at the amino acid level of 70%, preferably 80%, especially preferably of 90%, over the entire region of 5 the sequence shown in SEQ ID NO: 2 (Program PileUp, J. Mol. Evolution., 25, 351-360, 1987, Higgins et al., CABIOS, 5 1989: 151-153).
- 10 5. An amino acid sequence encoded by a nucleic acid sequence as claimed in claim 1.
6. A nucleic acid construct comprising a nucleic acid sequence as claimed in claim 1, wherein the nucleic acid sequence is linked to one or more regulatory signals. 15
7. The use of a nucleic acid sequence as claimed in claim 1 or of a nucleic acid construct as claimed in claim 6 for the generation of transgenic plants.
- 20 8. A vector comprising a nucleic acid sequence as claimed in claim 1 or a nucleic acid construct as claimed in claim 6.
9. A vector as claimed in claim 8, which is a linear or circular DNA, a phage, a virus, a transposon, an IS element, a 25 phasmid, a phagemid, a cosmid or a plasmid.
10. An organism comprising at least one nucleic acid sequence as claimed in claim 1, at least one nucleic acid construct as claimed in claim 6 or at least one vector as claimed in 30 claim 8.
11. An organism as claimed in claim 10, which is a eukaryotic organism.
- 35 12. An organism as claimed in claim 10 or 11, which is a plant, a eukaryotic microorganism or an animal.
13. An organism as claimed in any of claims 10 to 12, which is a plant, a fungus or a yeast. 40
14. An organism as claimed in any of claims 10 to 13, which is Yarrowia lypolytica [sic], Saccharomyces cereviseae [sic], Traustochytrium, Arabidopsis thaliana, Brassica napus or Linium [sic] usitatissimum.

15. A transgenic plant comprising a nucleic acid sequence as claimed in claim 1 or a nucleic acid construct as claimed in claim 6.

5 16. A method of targeting proteins involved in lipid or fatty acid biosynthesis into liposomes or lipid bodies, which comprises combining the protein-encoding nucleic acids and one of the following sequences to give a joint protein-encoding sequence:

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a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1,

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b) nucleic acid sequences which are derived from the nucleic acid sequence shown in SEQ ID NO: 1 as the result of the degeneracy of the genetic code,

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c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1 which encode polypeptides with the amino acid sequences shown in SEQ ID NO: 2 and which have at least 60% homology at the amino acid level,

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d) a nucleic acid sequence with the sequence shown in SEQ ID NO: 3 or the amino-terminal portion of the coding region of this sequence, and

and [sic] introducing the resulting sequence into a eukaryotic organism.

30 17. A method of targeting proteins involved in lipid or fatty acid biosynthesis into liposomes or lipid bodies, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct as claimed in claim 6 into an oil-producing organism.

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18. A method of producing fatty acids or lipids, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct as claimed in claim 6 into an oil-producing organism, growing this organism and isolating the oil contained in the organism.

40 19. A method of producing fatty acids, which comprises introducing at least one nucleic acid sequence as claimed in claim 1 or at least one nucleic acid construct as claimed in claim 6 into an oil-producing organism, growing this

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organism, isolating the oil contained in the organism and liberating the fatty acids.

20. A method as claimed in any of claims 16 to 19, wherein the
5 organism is a plant or a eukaryotic microorganism.

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